COVID-19 in France:

A detailed mathematical model from

June 2021 to September 2021

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Introduction

There are various kinds of coronaviruses, and some cause disease. One such coronavirus was identified in 2019: the novel severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), which caused the infamous pandemic. The first case of the Coronavirus Disease (COVID-19) was reported on December 1, 2019. The virus usually spreads through droplets and particles released into the air when an infected person breathes, talks, laughs, sings, coughs, and sneezes (What Is Coronavirus?, 2022). The symptoms appear in people within 2 to 14 days; they can remain contagious for up to 2 days before symptoms appear and then remain infectious for up to 10 to 20 days (depending on their immune system and the severity of their illness). This period is known as the incubation period for the virus. Some common symptoms include cough, fever or chills, shortness of breath, and the loss of taste or smell. However, it is possible to have COVID-19 and be asymptomatic (What Is Coronavirus?, 2022).

COVID-19 spread across the world rapidly and made its way from China to France within a month of the first-ever reported case of the virus. France was one of the European countries hardest hit by the COVID-19 pandemic. There was a direct connection between the first three cases, reported on January 24, 2020 (Or et al., 2021), in France and the Wuhan outbreak. By the end of the year 2020, France had one of the highest rates of prevalence in Europe, with over 2 million cases reported. France reported its first fatality in February 2020 (ENGLISH CORONAVIRUS: Key Numbers for COVID-19 and Its Evolution in France and Across the World, n.d.). Undoubtedly, France was as underprepared for the pandemic as many other countries worldwide. The pandemic brought out the limitations of the healthcare system and gave feedback on areas

of improvement for the country's system. The country benefits from a universal health insurance system and a centralised presidential regime with a strong public administration, which implies that swift and country-wide decisions can be made. It is also fully equipped with a relatively high number of healthcare professionals and hospital beds compared to many other European countries (Or et al., 2021).

Our chosen data was from June 2021 to September 2021, which includes the onset of the second wave, and starting in December 2020, vaccinations were getting approved, such as Pfizer/BioNTech, Oxford/AstraZeneca, and Johnson & Johnson (Tan-Lhernould et al., 2023). Our chosen period spans the population that is getting vaccinated daily. Moreover, by September 30, 2021, about 60% of the population in France was fully vaccinated (Antonini et al., 2021). To understand more about how France responded to the pandemic, we must also inspect the country's socioeconomic conditions. When the pandemic first hit Europe, France was focused on the political turmoil about the strikes against planned pension reform and the forthcoming local elections (Or et al., 2021). However, the country managed to tackle this unexpected virus in an organised manner. France integrated a four-stage national plan. The first stage included limiting international travel starting in February 2020. The second stage included banning large public gatherings and all visits to residential nursing homes. The third stage consisted of reducing the risk to frontline workers (hospital staff). All of this led to a national lockdown for nearly two months.

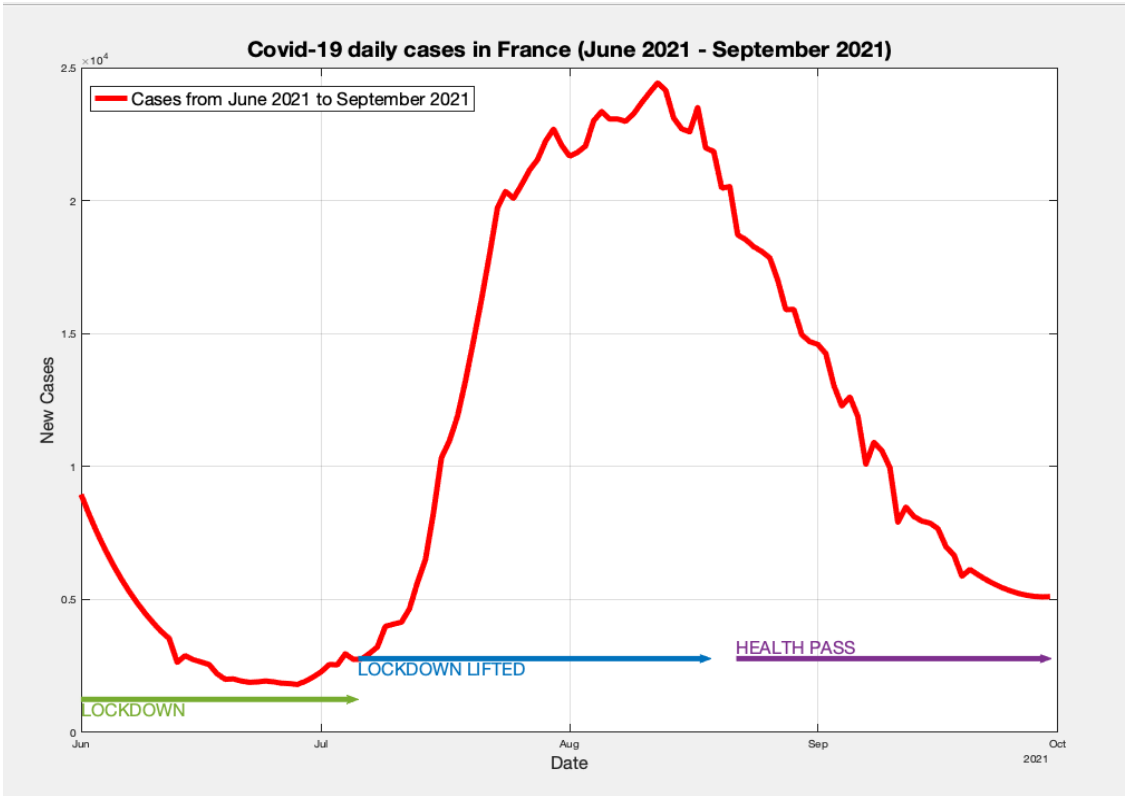

Figure 1 Data Set is chosen for forming the model for COVID-19 (Public Health Agency of Canada, 2024).

A slightly interesting fact is that France introduced a health pass during the summer of 2021 (The COVID-19 Vaccine Health Pass Fraud in France, 2022) to increase vaccination uptake and fight the surge of the Delta variant, which caused a significant decline in the cases (Figure 1).

Model

We decided to develop a four-compartment SVIR model, accounting for Susceptible – Vaccinated – Infectious – Recovered classifications of the population (Figure 2), which fits the data we are currently dealing with.

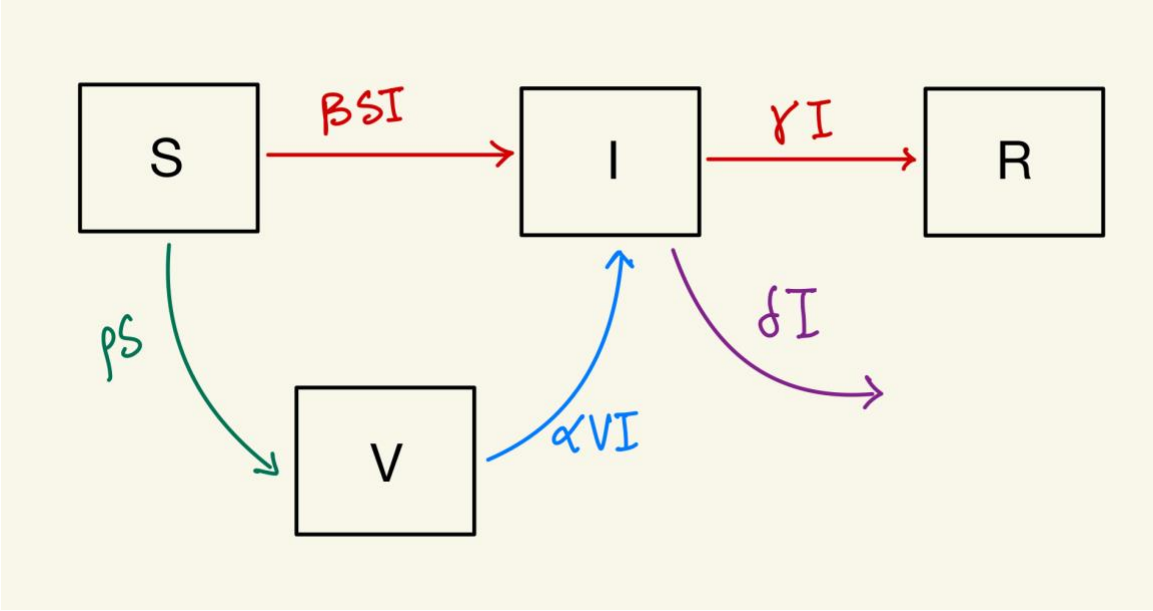

Figure 2 SVIR Model of COVID-19 in France from June 2021 to September 2021.

In the model, the S compartment contains the unvaccinated individuals during that time, and the V compartment contains the vaccinated individuals who are protected from the infection. The I compartment contains the individuals who are currently infected and can pass on the infection. The R compartment contains individuals who have recovered from COVID-19 and have immunity from the recent infection.

We define the model by the following differential equations:

$$\frac{dS}{dt} = -\beta SI - \rho S$$

$$\frac{dI}{dt} = \beta SI + \alpha VI - \delta I - \gamma I$$

$$\frac{dV}{dt} = \rho S - \alpha VI$$

$$\frac{dR}{dt} = \gamma I$$

This model is simpler than what we would expect to see for a realistic data set. However, given the data points that we have (122 points), it works out for the time being. Our model uses the mass-action mechanism of infection transmission. On reading the equations in the model diagram, we can explain what each constant signifies. Here β is the mass action constant, which can be defined as the rate at which the infection transmits from one person. Moving out of the S compartment, we see ρ the vaccination rate per capita of susceptible individuals. Our model also considers the possibility of Vaccinated people getting infected again at the rate of α per capita. Then, as seen in the past, COVID-19 caused quite a few fatalities, and our model takes this rate δ. Lastly, our model takes into consideration the number of people recovered from this infection, which is at the rate of γ.

In order to make everything work smoothly, our model makes some assumptions. Our assumptions are listed below:

- Constant Vaccination Rate
    - The vaccination rate (ρ) is assumed to be constant throughout the study period, implying no significant changes in vaccination policy, supply, or uptake over time.

- Negligible Deaths in Susceptible and Vaccinated Compartment
    - The death rate among susceptible S and vaccinated V individuals is negligible compared to deaths among the infected population I .
    - This simplifies the model by focusing on mortality effects only within the infected population.
- Constant Death Rate
    - The death rate (δ) of the infected individuals is taken constant,$\delta = \frac{1}{12} or\ 0.07\ (assumed)$, reflecting stable healthcare capacity and disease severity over the analysed period.
- Two-Week Infectious Period
    - The average infectious period is set to two weeks, aligning with the epidemiological studies on COVID-19 (Or et al., 2021).
    - The assumption is reflected in the active case computation as a 14-day rolling sum of new cases.
- Closed Population
    - The model assumes a closed population with no immigration, emigration or births during the study period (Or et al., 2021).
    - This ensures that population dynamics outside the scope of the disease are not affecting results
- No Waning Immunity
    - Recovered R individuals are assumed to have permanent immunity, with no transitions back to the susceptible compartment S during the study period.

- Homogenous Mixing
    - All individuals in the population are equally likely to interact, ignoring spatial or demographic heterogeneity.
- Vaccination Effectiveness
    - Vaccination is assumed to reduce susceptibility but not completely prevent infection (αVI) term in the model captures residual transmission among vaccinated individuals.
- Simplified Disease Dynamics
    - Disease progression within individuals is not explicitly modelled (e.g., asymptomatic vs symptomatic cases, hospitalisation, etc.), and all infected individuals are treated as equally infectious.
- Constant Transmission Rate (Mass action rate)
    - The transmission rate (β) is a random exponential function of time t that fluctuates according to the cases and gives an accurate fit for the data.

It is crucial to inform the reader that our model is imperfect, and it will give us the desired results if only we have an accurate model and the estimations are right in our analysis section. The attempt of this paper is to show the process of elimination, findings and intuitive thinking that goes on in making a disease model.

Analysis and Data Fitting

The Data was obtained from the Public Health Agency of Canada with the true number of daily new COVID-19 cases reported. There were certain dips and noise in data that were manipulated to make it fit the model. Our time frame spanned from June 2021 to September 2021.

We also calculated the number of active cases for a selected time frame from July 1st 2021 to September 30th 2021 (Figure 3)

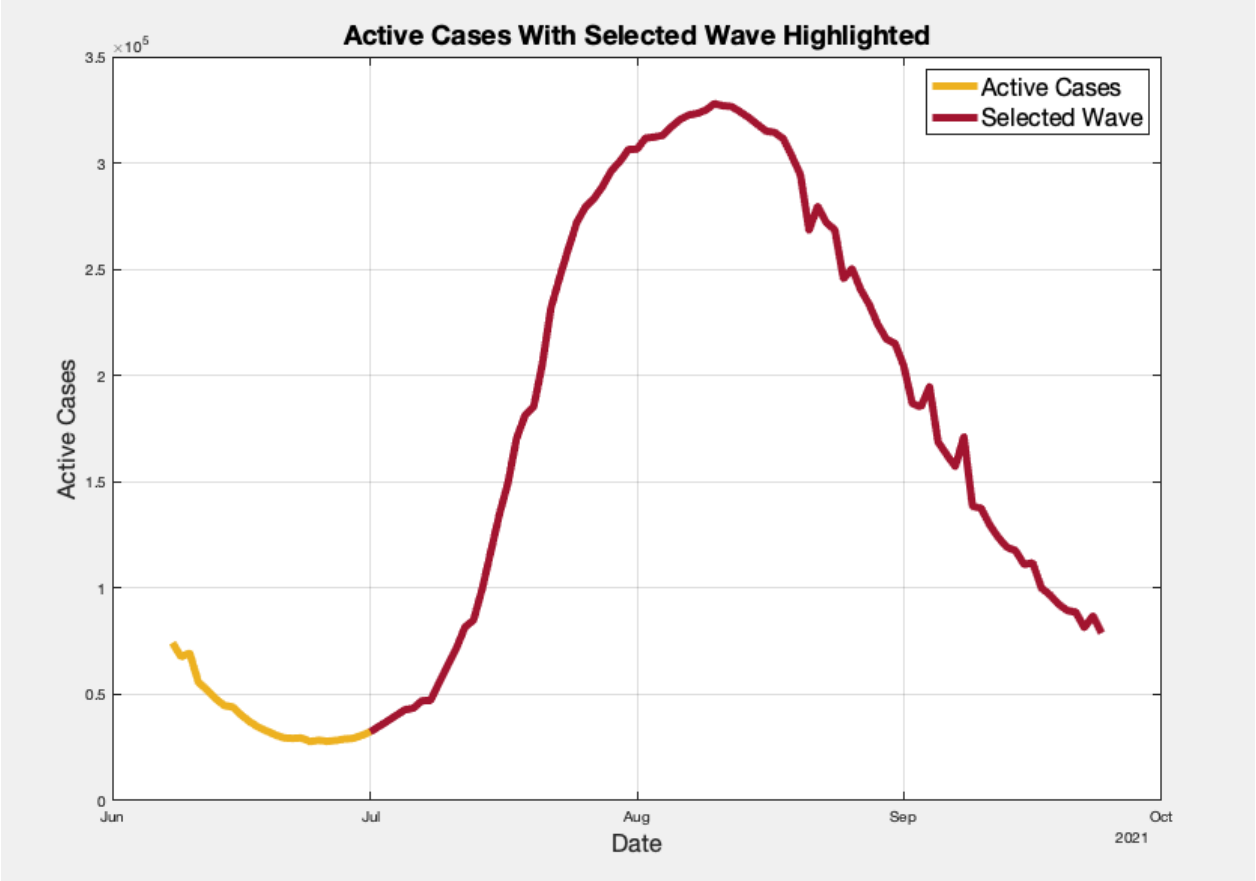

Figure 3 Selected wave of active cases where there is most fluctuation of cases

Exponential Growth and Decay

A period of exponential growth was observed from 1st July 2021 to 15th August 2021, and a period of exponential decay from 16th August 2021 to 24th September. This was an estimation from observing data by eye. This is easier to show through plots; we used the polyfit function in MATLAB to show the best-fit line for the active cases (figure 4).

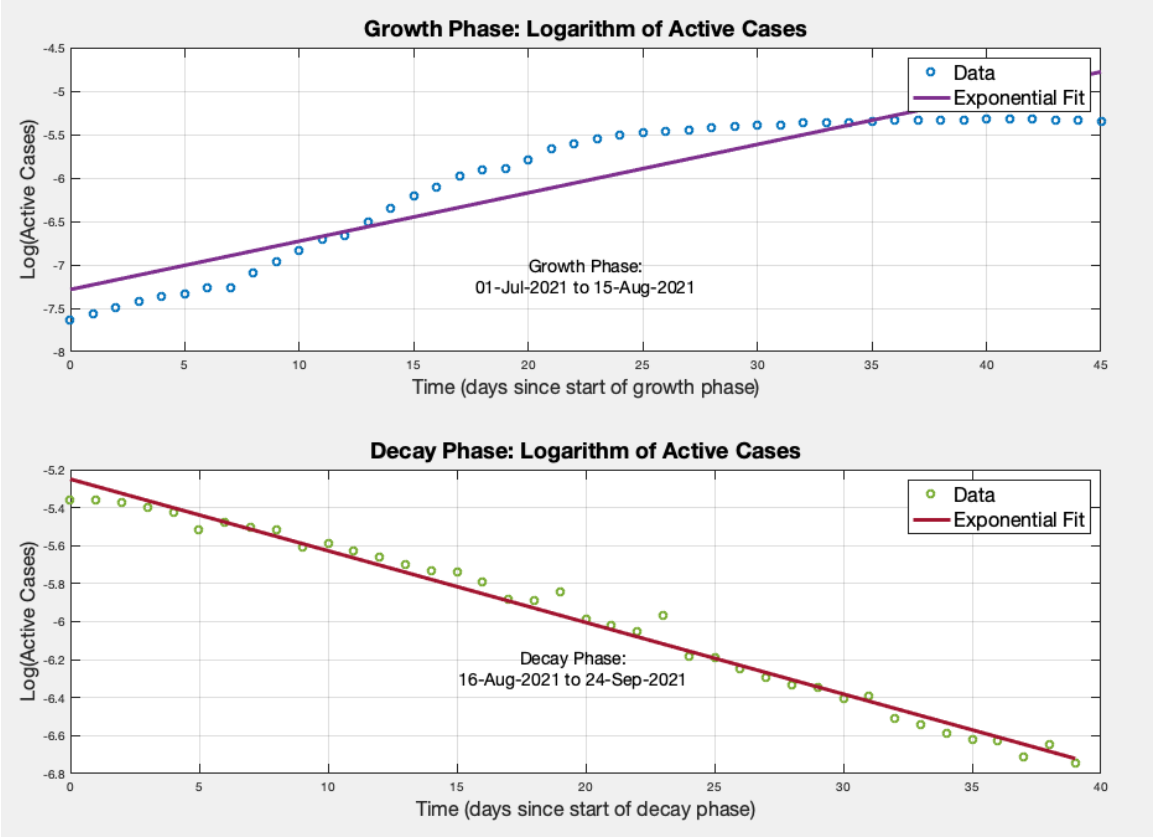

Figure 4 Top: Exponential Growth

Bottom: Exponential Decay

From these graphs, we were able to use MATLAB again to find the Doubling time and half-life of the infectious period in this time frame.

Calculation of half-life:

$$t \approx 18.3873$$

This number is significant because the half-life determines the active infectious cases of COVID-19 halved approximately every 18 days from July 1st, 2021, till August 15th, 2021.

Calculating the Doubling time:

$$t \approx 12.4502$$

The Doubling time during this period determines the active infectious cases of covid 19 doubled approximately every 13 days from August 16th, 2021, till September 24th, 2021.

Equilibrium States

Our model assumes that all parameters are non-negative. $\beta,\ \alpha,\ \gamma, \delta\ and\ \rho$ are all constants.

Nullclines:

For S:

$$\frac{dS}{dt} = 0 \implies -\beta SI - \rho S = 0$$

$$\implies S(-\beta I - \rho) = 0 \implies S = 0$$

$$\boldsymbol{or}$$

$$I = -\frac{\rho}{\beta}$$

For I:

$$\frac{dI}{dt} = 0 \implies \beta SI + \alpha VI - \delta I - \gamma I = 0$$

$$\implies I(\beta S + \alpha V - \delta - \gamma) = 0$$

$$\implies I = 0$$

$$or$$

$$\implies \beta S + \alpha V = \delta + \gamma$$

For V:

$$\frac{dV}{dt} = 0 \implies \rho S - \alpha V I = 0$$

$$\implies V(\rho S - \alpha V) = 0$$

$$\implies V = 0$$

$$or$$

$$\implies \rho S = \alpha V I$$

For R:

$$\frac{dR}{dt} = 0 \implies \gamma I = 0 \implies I = 0$$

Jacobian Matrix for the system:

$$\frac{\boldsymbol{dS}}{\boldsymbol{dt}} = -\boldsymbol{\beta SI} - \boldsymbol{\rho S}$$

$$\frac{\boldsymbol{dI}}{\boldsymbol{dt}} = \boldsymbol{\beta SI} + \boldsymbol{\alpha VI} - \boldsymbol{\delta I} - \boldsymbol{\gamma I}$$

$$\frac{\boldsymbol{dV}}{\boldsymbol{dt}} = \boldsymbol{\rho S} - \boldsymbol{\alpha VI}$$

$$\frac{\boldsymbol{dR}}{\boldsymbol{dt}} = \boldsymbol{\gamma I}$$

Above are the four equations that we use to calculate the Jacobian, It is the matrix of the partial derivatives (w.r.t S, I, V, R) of the equations of the system given above.

$$J =$$

$$\begin{bmatrix} \frac{\partial}{\partial S}(-\beta SI - \rho S) & \frac{\partial}{\partial I}(-\beta SI - \rho S) & \frac{\partial}{\partial V}(-\beta SI - \rho S) & \frac{\partial}{\partial R}(-\beta SI - \rho S) \\ \frac{\partial}{\partial S}(\beta SI + \alpha VI - \delta I - \gamma I) & \frac{\partial}{\partial I}(\beta SI + \alpha VI - \delta I - \gamma I) & \frac{\partial}{\partial V}(\beta SI + \alpha VI - \delta I - \gamma I) & \frac{\partial}{\partial R}(\beta SI + \alpha VI - \delta I - \gamma I) \\ \frac{\partial}{\partial S}(\rho S - \alpha VI) & \frac{\partial}{\partial I}(\rho S - \alpha VI) & \frac{\partial}{\partial V}(\rho S - \alpha VI) & \frac{\partial}{\partial R}(\rho S - \alpha VI) \\ \frac{\partial}{\partial S}(\gamma I) & \frac{\partial}{\partial I}(\gamma I) & \frac{\partial}{\partial V}(\gamma I) & \frac{\partial}{\partial R}(\gamma I) \end{bmatrix}$$

$$J = \begin{bmatrix} -\beta I - \rho & -\beta S & 0 & 0 \\ \beta I & \beta S + \alpha V - \delta - \gamma & \alpha I & 0 \\ \rho & -\alpha V & -\alpha I & 0 \\ 0 & \gamma & 0 & 0 \end{bmatrix}$$

Moving forward with the Jacobian calculated. We can compute the equilibriums of the system:

Trivial Equilibrium

The trivial equilibrium occurs at (S, I, V, R) = (0, 0, 0, 0) = E_0

$$J|_{E_0} = \begin{bmatrix} -\rho & 0 & 0 & 0 \\ 0 & -\delta - \gamma & 0 & 0 \\ \rho & 0 & 0 & 0 \\ 0 & \gamma & 0 & 0 \end{bmatrix}$$

Using appropriate MATLAB code and tools. The eigenvalues of this matrix are as follows:

$$\lambda_1 = -\rho$$

$$\lambda_2 = -\delta - \gamma$$

$$\lambda_3 = 0 \ (with\ multplicity\ 2)$$

At $\lambda_1 = -\rho < 0\ because\ \rho > 0$

At $\lambda_2 = -\delta - \gamma < 0\ because\ \delta > 0\ and\ \gamma > 0$

Moreover, two zero eigenvalues ($\lambda_3 = 0$) indicate **neutral stability** at the trivial equilibrium.

Disease Free Equilibrium (DFE)

At the disease-free equilibrium (I = 0):

$$\frac{\boldsymbol{dS}}{dt} = \mathbf{0}, \frac{\boldsymbol{dV}}{dt} = \mathbf{0}, \frac{\boldsymbol{dR}}{dt} = \mathbf{0}$$

From $\frac{dS}{dt} = \mathbf{0}$:

$$-\beta SI - \rho S = 0 \implies S = \frac{\rho}{\rho}$$

$$E_{DFE} = (S, 0,0,0)$$

Endemic Equilibrium

The endemic equilibrium exists when the disease persists in the population. ($I \neq 0$)

$$\frac{\boldsymbol{dS}}{dt} = \mathbf{0}, \frac{\boldsymbol{dI}}{dt} = \mathbf{0}, \frac{\boldsymbol{dV}}{dt} = \mathbf{0}, \frac{\boldsymbol{dR}}{dt} = \mathbf{0}$$

From $\frac{dS}{dt} = -\beta SI - \rho S = 0$:

$$S(-\beta I - \rho) = 0 \implies S = 0 \; or \; I = -\rho\beta$$

Since $I \geq 0, \; S = 0$ it is not viable for an endemic equilibrium, so $S > 0$

From $\frac{\boldsymbol{dI}}{dt} = \boldsymbol{\beta SI + \alpha VI - \delta I - \gamma I = 0}$:

$$I(\beta S + \alpha V - \delta - \gamma) = 0$$

$$Since \; I \neq 0 \; we \; have:$$

$$\beta S + \alpha V = \delta + \gamma$$

From $\frac{dV}{dt} = \rho S - \alpha VI = 0$:

$$\rho S = \alpha VI \implies V = \frac{\rho S}{\alpha I}$$

From $\frac{dR}{dt} = \gamma I = 0$:

$$R = any\ constant(depends\ on\ total\ population\ constraints)$$

After performing all the necessary calculations, we are left with the *Endemic Equilibrium*:

$$\boldsymbol{E_{endemic}} = (\boldsymbol{S}^*, \boldsymbol{I}^*, \boldsymbol{V}^*, \boldsymbol{R}^*),$$

Where:

$$S = \frac{I(\delta + \gamma)}{\beta I + \rho}, V = \frac{\rho(\delta + \gamma)}{\alpha(\beta I * + \rho)},$$

And $\boldsymbol{R}^*$ depends on the total population constraint.

The stability of the Endemic Equilibrium can be given by the Jacobian Matrix:

$$J|_{endemic} = \begin{bmatrix} -\beta I^* - \rho & -\beta S^* & 0 & 0 \\ \beta I^* & \beta S^* + \alpha V^* - \delta - \gamma & \alpha I^* & 0 \\ \rho & \alpha V^* & \alpha I^* & 0 \\ 0 & \gamma & 0 & 0 \end{bmatrix}$$

Data Fitting of the Model and Parameter fitting

Given the model's simplicity, we made quite low estimates of our parameters. After developing the function "infectious_model" for our MATLAB code, it was necessary to fit some errors in the data as well (using the sum of squared errors (SSE)). This was done using the fminsearch function of MATLAB, which also helped us find the best fit for each fitted parameter and initial conditions.

$$I_0 = number\ of\ active\ cases\ from\ the\ selected\ wave$$

$$V_0 = 0.001$$

$$R_0 = 0$$

$$S_0 = 1 - I_0 - V_0 - R_0$$

The function "infectious_model" uses MATLAB's ode45 solver to fit the model to the data, the "fit_errors" function computed the SSE and minimised it (Figure 5).

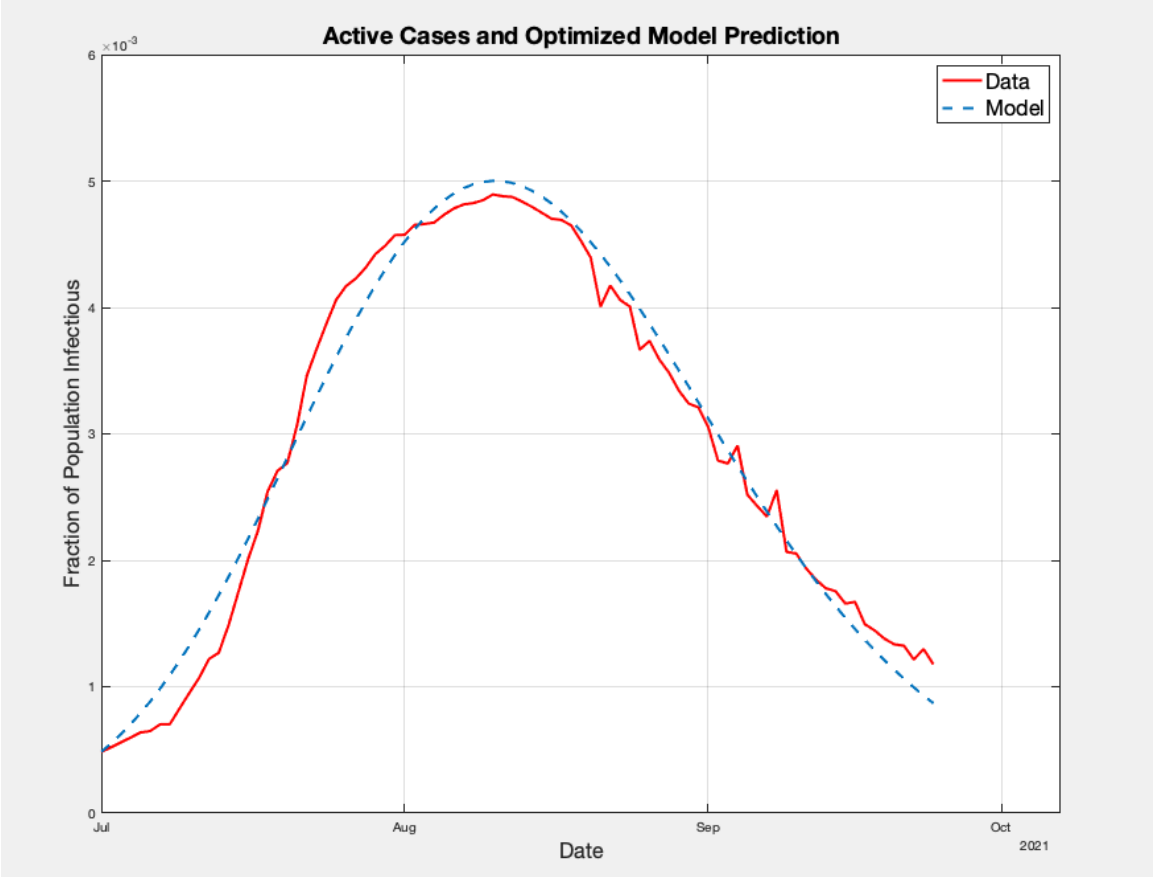

Figure 5 Best-fit curve using our model against the data we used

Some best-fit parameters from the model are as follows:

Best-Fit Parameters:

β (Transmission Rate): 0.12486

ρ(Vaccination Rate): 0.01789

α(Vaccinated Transmission Rate): -0.12883

γ(Recovery Rate): -0.34343

δ(Death Rate): 0.33674

Sensitivity Analysis

The sensitivity analysis evaluates the robustness of a model by introducing variability, here noise, into the input data, and we observe the resulting changes in the parameter estimates.

This provides more insight into the stability of the parameter fitting process and identifies which parameters are the most sensitive to uncertainties in the data.

Our objective was to determine how the variations in the observed data affected the best-fit parameters of the model and to assess the reliability of the model-fitting process.

Using MATLAB, we added Gaussian Noise ($N(0, \sigma)$) to the observed data to simulate stability. The noise level was set to 5% of the observed value ($\sigma = 0.05 * data$). We generated a total of 20 noisy datasets.

The fitting process was repeated using the same optimisation method (fminsearch). Then, the best-fit parameters were recorded for each noisy dataset (Figure 6).

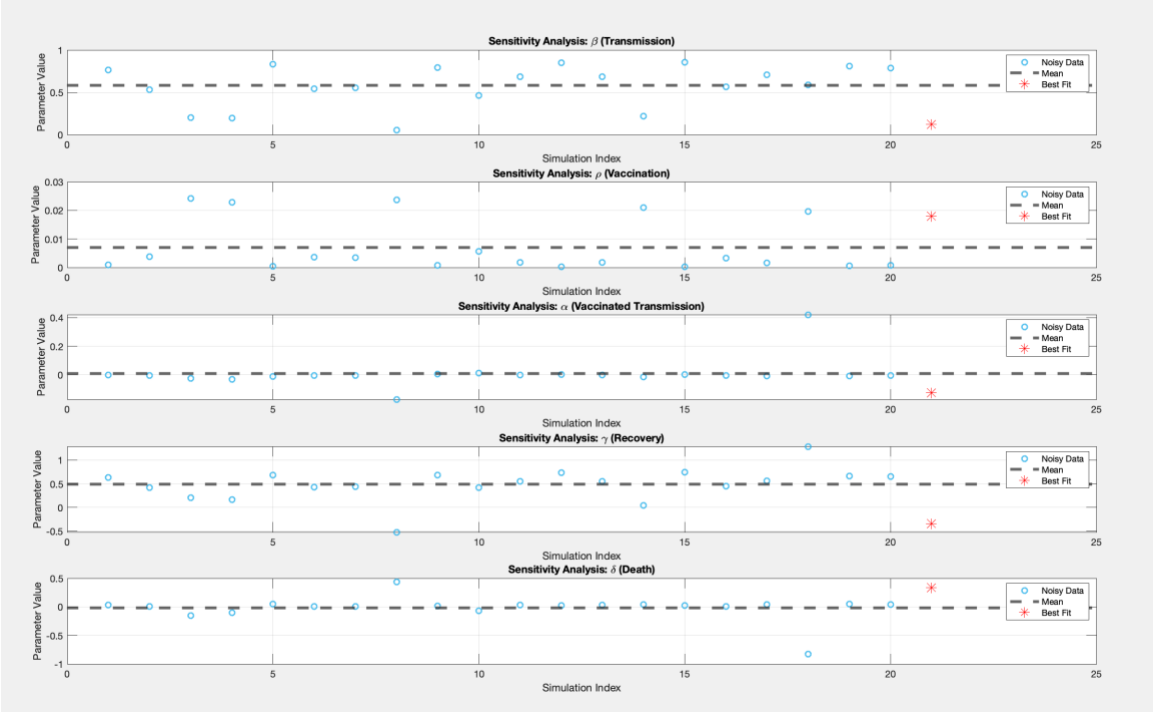

Figure 6 Sensitivity analysis of each parameter

Reproduction Number (R_0)

We calculated the R_0 value from our model, which gave us the following formula:

$$R_0 = \frac{\beta}{\gamma + \delta}$$

We obtain this value by multiplying the average number of days spent infection $\frac{1}{\gamma+\delta}$ with the average number of infections per infectious individual βS. However, on comparing to literature values, we estimated in a range of [2.5, 3.0], our computed $R_0 = -18.6504$, , which is in disagreement with the literature values. We discovered that this may be because the cases might be underreported, our assumptions in the model (e.g., constant parameters, homogenous mixing, etc.) may differ from reality, the data set may not

represent the full range of transmission dynamics or even noise or inconsistencies in the dataset used for the model fitting can cause this huge error.

Conclusions

France had a great healthcare system, and they tackled the virus efficiently. The onset of summer led to the introduction of the Health Pass, which declined the number of reported cases till the end of June, along with the lockdown in place. However, lifting the lockdown causes a surge in cases even after vaccinations and health passes. Our model does a good job of identifying exponential growth and decay in the selected period of July 1st, 2021, to September 30th, 2021. It also suggests that constant vaccination will eventually lead to a decline in the number of reported cases.

Our results incorporate factors of lockdowns and health passes being in play and report a half-life, which estimates the approximate fit of the reported data. In the sensitivity analysis, we report these estimated parameters that are best fit to our model given the assumptions we have made. It does not meet the actual reported data. Our model fits most of the variations seen in the reported cases over just a few months.

Critical Overview

In retrospect, our model is good for a first layout of the pandemic faced by France. However, it is deeply flawed in its estimations and retrieving the reproductive ratio for the data we used. Our assumptions for the model could have been more intuitive and pragmatic considering the conditions of the country regarding policy change, mask mandates, vaccination variability and much more.

The introduction of new parameters and even compartments could have helped achieve improved results. We must make note of the errors that are in our model. The assumptions made do not match the realistic outcome, and there were a lot of trials and errors done to get some best-fit parameters for the model. Initial conditions were repeatedly modified and made to fit the model. The learning outcome from this analysis is that our analysis and model could have turned out to be much more accurate and realistic if we had more time and resources to refer to the values that were calculated. A model with more parameters, better initial conditions and assumptions would have given us results that fit the actual data accurately.

References

What Is Coronavirus? (2022, July 29). Johns Hopkins Medicine. https://www.hopkinsmedicine.org/health/conditions-and-diseases/coronavirus

Or, Z., Gandré, C., Zaleski, I. D., & Steffen, M. (2021). France's response to the Covid-19 pandemic: between a rock and a hard place. *Health Economics Policy and Law*, *17*(1), 14–26. https://doi.org/10.1017/s1744133121000165

ENGLISH CORONAVIRUS : Key numbers for COVID-19 and its evolution in France and worldwide. (n.d.). https://www.santepubliquefrance.fr/dossiers/coronavirus-covid-19/english-coronavirus-key-numbers-for-covid-19-and-its-evolution-in-france-and-across-the-world

Antonini, M., Eid, M. A., Falkenbach, M., Rosenbluth, S. T., Prieto, P. A., Brammli-Greenberg, S., McMeekin, P., & Paolucci, F. (2021). An analysis of the COVID-19 vaccination campaigns in France, Israel, Italy and Spain and their impact on health and economic outcomes. *Health Policy and Technology*, *11*(2), 100594. https://doi.org/10.1016/j.hlpt.2021.100594

Tan-Lhernould, L., Tamandjou, C., Deschamps, G., Platon, J., Sommen, C., Chereau, F., Du Châtelet, I. P., Cauchemez, S., Vaux, S., & Paireau, J. (2023). Impact of vaccination against severe COVID-19 in the French population aged 50 years and above a retrospective population-based study. *BMC Medicine*, *21*(1). https://doi.org/10.1186/s12916-023-03119-8

Public Health Agency of Canada. (2024, October 22). *Health Infobase - Health data in Canada*. Canada.ca. https://health-infobase.canada.ca/

The COVID-19 vaccine health pass fraud in France. (2022, March 27). Clinical Microbiology and Infection. https://doi.org/10.1016/j.cmi.2022.04.006